STIC-Biotech/ChemLib 178329 MG

From: Chan, Christina
Sent: Wednesday, February 01, 2006 10:41 AM
To: Sullivan, Daniel; STIC-Biotech/ChemLib
Subject: RE: Rush sequence search 09/886942

Please rush! Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Sullivan, Daniel
Sent: Wednesday, February 01, 2006 7:13 AM
To: Chan, Christina
Subject: Rush sequence search 09/886942

Hi Chris,

Please approve the following search for an after final amended case. Thanks.

Please search for the following in the pending, issued patent and commercial databases:

A nucleic acid comprising SEQ ID NO: 8;
a nucleic acid comprising the sequence from position 1 to position 909 of SEQ ID NO: 8;
a nucleic acid comprising the sequence from position 1 to position 932 of SEQ ID NO: 21.

Thank you.

Daniel M. Sullivan
Examiner AU 1636
Remsen Bldg.
Room 2A74
Tel: (571) 272-0779
Mailbox: 2C70

****
Searcher: Jan
Searcher Phone: 27504
Date Searcher Picked up: 2/2/06
Date completed: 2/6/06
Searcher Prep Time: 1Y
Online Time: 15

****
Type of Search
NA# ✓ AA#:
S/L: Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

****
Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: ✓
WWW/Internet:
Other (Specify):

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 11:13:43 ; Search time 233.045 Seconds
(without alignments)
7291.426 Million cell updates/sec

Title: US-09-886-942-8_COPY_1_909
Perfect score: 909
Sequence: 1 atatgaggctatatcgccga.....aacggtgcattggaacgcgg 909

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3446060 seqs, 934668629 residues

Total number of hits satisfying chosen parameters: 6892120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*
12: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	891.4	98.1	1848	1	PCT-US05-42058-60	Sequence 60, Appl
2	864.4	95.1	8687	11	US-11-297-317-15	Sequence 15, Appl
3	864.4	95.1	8687	11	US-11-297-317-16	Sequence 16, Appl
4	864.4	95.1	9362	11	US-11-297-317-18	Sequence 18, Appl
5	864.4	95.1	9400	11	US-11-297-317-17	Sequence 17, Appl
6	810.2	89.1	5041	11	US-11-296-119-6	Sequence 6, Appli
7	810.2	89.1	5043	11	US-11-296-119-5	Sequence 5, Appli
8	810.2	89.1	5101	11	US-11-296-119-4	Sequence 4, Appli
9	810.2	89.1	5924	11	US-11-296-119-3	Sequence 3, Appli
10	810.2	89.1	5982	11	US-11-296-119-2	Sequence 2, Appli
11	810.2	89.1	6233	11	US-11-296-119-10	Sequence 10, Appl
12	810.2	89.1	17402	11	US-11-296-119-8	Sequence 8, Appli
13	810.2	89.1	18116	11	US-11-296-119-7	Sequence 7, Appli
14	787	86.6	4207	6	US-10-947-881A-4	Sequence 4, Appli
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16	787	86.6	4210	6	US-10-947-881A-5	Sequence 5, Appli
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18	787	86.6	6255	6	US-10-947-881A-13	Sequence 13, Appl
19	787	86.6	6255	7	US-10-947-881A-13	Sequence 13, Appl
20	786.4	86.5	8255	6	US-10-334-235A-17	Sequence 17, Appl
21	786.4	86.5	8255	7	US-10-334-235A-17	Sequence 17, Appl
22	786.4	86.5	9100	6	US-10-334-235A-16	Sequence 16, Appl
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26	779	85.7	3893	11	US-11-009-063-3	Sequence 3, Appli
c 27	779	85.7	3893	11	US-11-009-063-39	Sequence 39, Appl
28	779	85.7	3894	11	US-11-009-063-1	Sequence 1, Appli
c 29	779	85.7	3894	11	US-11-009-063-37	Sequence 37, Appl
30	755	83.1	9918	11	US-11-009-063-5	Sequence 5, Appli
31	734	80.7	4006	11	US-11-274-814-11	Sequence 11, Appl
32	734	80.7	6630	9	US-11-238-171-51	Sequence 51, Appl
33	732.2	80.6	7354	9	US-11-327-232-1	Sequence 1, Appli
34	728.8	80.2	8908	11	US-11-204-755-12	Sequence 12, Appl
35	712.8	78.4	750	5	US-09-965-697A-3	Sequence 3, Appli
36	690.4	76.0	7006	11	US-11-295-006-1	Sequence 1, Appli
37	678.6	74.7	2947	11	US-11-009-063-2	Sequence 2, Appli
c 38	678.6	74.7	2947	11	US-11-009-063-38	Sequence 38, Appl
39	674.4	74.2	684	1	PCT-US05-42058-69	Sequence 69, Appl
40	664	73.0	9545	11	US-11-009-063-4	Sequence 4, Appli
41	660.6	72.7	9380	6	US-10-554-181-5	Sequence 5, Appli
42	660.6	72.7	9380	7	US-10-554-181-5	Sequence 5, Appli
43	660.6	72.7	9490	6	US-10-554-181-7	Sequence 7, Appli
44	660.6	72.7	9490	7	US-10-554-181-7	Sequence 7, Appli
45	660.6	72.7	10086	6	US-10-554-181-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
PCT-US05-42058-60
; Sequence 60, Application PC/TUS0542058
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Kyrkanides, Stephanos
; APPLICANT: O'Banion, M. Kerry
; TITLE OF INVENTION: INFLAMMATION MODELS IN NEURODEGENERATIVE
; TITLE OF INVENTION: AND ARTHRITIC DISORDERS
; FILE REFERENCE: 21108.0046P1
; CURRENT APPLICATION NUMBER: PCT/US05/42058
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: 60/646,097
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/627,604
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
PCT-US05-42058-60

Query Match 98.1%; Score 891.4; DB 1; Length 1848;
Best Local Similarity 98.8%; Pred. No. 1.8e-260;
Matches 898; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy        121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCCGTATCATAATATGTACATTTAT 180
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Qy        181 ATTGGCCCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 11:01:54 ; Search time 5767.16 Seconds
(without alignments)
8714.867 Million cell updates/sec

Title: US-09-886-942-8_COPY_1_909
Perfect score: 909
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		909	100.0	1767	34	US-09-886-942-8	Sequence 8, Appli
2		909	100.0	3879	51	US-10-446-629-2	Sequence 2, Appli
3		909	100.0	4790	51	US-10-446-629-3	Sequence 3, Appli
4		899.4	98.9	1767	34	US-09-886-942-21	Sequence 21, Appl
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6	c	899.4	98.9	233076	61	US-10-756-114-1	Sequence 1, Appli
7	c	899.4	98.9	233076	61	US-10-757-349-1	Sequence 1, Appli
8		897.8	98.8	6408	39	US-09-996-128A-1	Sequence 1, Appli
9		897.8	98.8	6485	39	US-09-996-128A-2	Sequence 2, Appli
10		893	98.2	1767	34	US-09-886-942-5	Sequence 5, Appli
11		893	98.2	1767	34	US-09-886-942-15	Sequence 15, Appl
12		893	98.2	1767	34	US-09-886-942-16	Sequence 16, Appl
13		891.4	98.1	1848	1	PCT-US02-29640-51	Sequence 51, Appl
14		891.4	98.1	1848	1	PCT-US03-13672-32	Sequence 32, Appl
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17		891.4	98.1	1848	64	US-10-978-927-32	Sequence 32, Appl
18		891.4	98.1	6845	43	US-10-239-804-6	Sequence 6, Appli
19		891.4	98.1	6845	62	US-10-838-906-26	Sequence 26, Appl
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21		891.4	98.1	7073	14	US-08-480-120-15	Sequence 15, Appl
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 11:01:54 ; Search time 11210.8 Seconds
(without alignments)
8714.867 Million cell updates/sec

Title: US-09-886-942-8
Perfect score: 1767
Sequence: 1 atatgaggctatatcgccga.....tttctgcagtcaccgtcctt 1767

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	4	1741.4	98.6	1767	34	US-09-886-942-21	Sequence 21, Appl
c	5	1741.4	98.6	218802	62	US-10-897-508-1	Sequence 1, Appli
c	6	1741.4	98.6	233076	61	US-10-756-114-1	Sequence 1, Appli
c	7	1741.4	98.6	233076	61	US-10-757-349-1	Sequence 1, Appli
	8	1737.8	98.3	6408	39	US-09-996-128A-1	Sequence 1, Appli
	9	1737.8	98.3	6485	39	US-09-996-128A-2	Sequence 2, Appli
	10	1728.6	97.8	1767	34	US-09-886-942-5	Sequence 5, Appli
	11	1728.6	97.8	1767	34	US-09-886-942-15	Sequence 15, Appl
	12	1727	97.7	1767	34	US-09-886-942-16	Sequence 16, Appl
	13	1725.4	97.6	1767	34	US-09-886-942-14	Sequence 14, Appl
	14	1720.6	97.4	1767	34	US-09-886-942-18	Sequence 18, Appl
	15	1714.2	97.0	1765	34	US-09-886-942-13	Sequence 13, Appl
c	16	1699.8	96.2	235671	61	US-10-756-114-2	Sequence 2, Appli
c	17	1699.8	96.2	235671	61	US-10-757-349-2	Sequence 2, Appli
	18	1698.8	96.1	1766	34	US-09-886-942-6	Sequence 6, Appli
	19	1695.2	95.9	8251	52	US-10-521-768-2	Sequence 2, Appli
	20	1695.2	95.9	13254	40	US-10-016-986-156	Sequence 156, App
c	21	1695.2	95.9	13254	40	US-10-016-986-170	Sequence 170, App
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

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(without alignments)
7291.426 Million cell updates/sec

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Perfect score: 1767
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3446060 seqs, 934668629 residues

Total number of hits satisfying chosen parameters: 6892120

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1411.8	79.9	9287	11	US-11-301-309-20	Sequence 20, Appl
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17	810.2	45.9	6233	11	US-11-296-119-10	Sequence 10, Appl
18	810.2	45.9	17402	11	US-11-296-119-8	Sequence 8, Appli
19	810.2	45.9	18116	11	US-11-296-119-7	Sequence 7, Appli
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; Sequence 3, Application US/11009063
; GENERAL INFORMATION:
; APPLICANT: Robinson, Harriet L.
; APPLICANT: Amara, Rama
; APPLICANT: Ross, Ted M.
; APPLICANT: Bright, Rick A.
; TITLE OF INVENTION: DNA EXPRESSION VECTORS AND METHODS OF USE
; FILE REFERENCE: 12804-005003
; CURRENT APPLICATION NUMBER: US/11/009,063
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: US 60/186,364
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/251,083
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/798,675
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 46
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; SEQ ID NO 3
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; OTHER INFORMATION: vaccine vector pGA3
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)...(690)
; OTHER INFORMATION: cytomegalovirus intermediate early promoter
US-11-009-063-3

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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

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Perfect score: 1767
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	6	1737.8	98.3	6408	3	US-09-996-128A-1	Sequence 1, Appli
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	10	1727	97.7	1767	3	US-09-886-942-16	Sequence 16, Appl
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	12	1720.6	97.4	1767	3	US-09-886-942-18	Sequence 18, Appl
	13	1714.2	97.0	1765	3	US-09-886-942-13	Sequence 13, Appl
	14	1698.8	96.1	1766	3	US-09-886-942-6	Sequence 6, Appli
	15	1695.2	95.9	13254	6	US-10-016-986-156	Sequence 156, App
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	17	1692.8	95.8	2170	3	US-09-977-066-4	Sequence 4, Appli
	18	1692.8	95.8	2170	10	US-11-103-805-4	Sequence 4, Appli
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	24	1620.6	91.7	13464	7	US-10-394-388A-9	Sequence 9, Appli
	25	1620.4	91.7	6845	5	US-10-239-804-6	Sequence 6, Appli
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	27	1619	91.6	3893	3	US-09-798-675-3	Sequence 3, Appli
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	40	1606.2	90.9	4945	5	US-10-149-640-9	Sequence 9, Appli
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ALIGNMENTS

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; Patent No. US20020081708A1
; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA
; WRIGHT, ANNE
; SEMYONOV, ANDREY
; APPLICANT:
; TITLE OF INVENTION: NOVEL CHIMERIC PROMOTERS
; FILE REFERENCE: 02-031910US
; CURRENT APPLICATION NUMBER: US/09/886,942
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/213,829
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 40
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-886-942-8

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Best Local Similarity 100.0%; Pred. No. 0;
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

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Perfect score: 1767
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1767	100.0	3879	13	ADS20069	Ads20069 pMV10.1-s
3	1767	100.0	4790	13	ADS20070	Ads20070 pMV10.1-C
4	1741.4	98.6	1767	6	AAL38393	Aal38393 Consensus
c 5	1741.4	98.6	218802	14	ADW98820	Adw98820 Human her
6	1737.8	98.3	6408	8	ABX10643	Abx10643 Vector, h
7	1737.8	98.3	6485	8	ABX10644	Abx10644 Vector, h
8	1728.6	97.8	1767	6	AAL38377	Aal38377 Chimeric
9	1728.6	97.8	1767	6	AAL38387	Aal38387 Chimeric
10	1727	97.7	1767	6	AAL38388	Aal38388 Chimeric
11	1725.4	97.6	1767	6	AAL38386	Aal38386 Chimeric
12	1720.6	97.4	1767	6	AAL38390	Aal38390 Chimeric
13	1720.6	97.4	1767	6	AAL38373	Aal38373 Chimeric
14	1714.2	97.0	1765	6	AAL38385	Aal38385 Chimeric
15	1698.8	96.1	1766	6	AAL38378	Aal38378 Chimeric
16	1695.2	95.9	8251	12	ADJ57065	Adj57065 Vector pl
17	1695.2	95.9	9831	14	AEB86488	Aeb86488 LAP vecto
18	1695.2	95.9	11795	3	AAA59345	Aaa59345 Nucleotid
19	1695.2	95.9	13254	2	AAT40915	Aat40915 Nucleotid
20	1695.2	95.9	13254	3	AAA32151	Aaa32151 pEe12 Com
c 21	1695.2	95.9	13254	3	AAA32165	Aaa32165 Complete
c 22	1695.2	95.9	13254	3	AAA31039	Aaa31039 Complete
23	1695.2	95.9	13535	12	ADJ57067	Adj57067 Vector pl
c 24	1695.2	95.9	229354	6	ABQ74179	Abq74179 Human cyt
25	1694.8	95.9	2133	1	AAN91042	Aan91042 Promoter-
26	1693.6	95.8	7073	2	AAT50962	Aat50962 TF8-5G9 C
27	1692.8	95.8	2170	6	AAD38152	Aad38152 Human cyt
28	1692.8	95.8	2361	8	ADA50595	Ada50595 HCMV imme
29	1692.8	95.8	2361	14	ADW07232	Adw07232 DNA seque
30	1692	95.8	7864	2	AAT50963	Aat50963 TF8-5G9 C
31	1691.2	95.7	1765	6	AAL38392	Aal38392 Wild-type
32	1688.8	95.6	13254	3	AAA31025	Aaa31025 pEe12 Com
33	1681.6	95.2	1767	6	AAL38391	Aal38391 Wild-type
34	1669.8	94.5	1757	6	AAL38389	Aal38389 Chimeric
35	1665	94.2	1757	6	AAL38383	Aal38383 Chimeric
36	1660.6	94.0	1758	6	AAL38374	Aal38374 Chimeric
37	1621.4	91.8	8911	12	ADN07735	Adn07735 Expressio
38	1620.6	91.7	4326	4	AAD04044	Aad04044 pWRG7077
39	1620.6	91.7	13464	12	ADK15560	Adk15560 Hantaan/A
40	1620.4	91.7	6845	6	ABK37491	Abk37491 Vesicular
41	1617.4	91.5	4282	4	AAF83668	Aaf83668 pCMV-II n
42	1617.4	91.5	7807	12	ADK15558	Adk15558 Hantaan h
43	1617.4	91.5	7913	12	ADK15559	Adk15559 Andes han
44	1616.4	91.5	3894	6	AAS19256	Aas19256 DNA vacci
45	1611.4	91.2	1715	6	AAL38379	Aal38379 Chimeric

ALIGNMENTS

RESULT 1
AAL38380
ID AAL38380 standard; DNA; 1767 BP.
XX
AC AAL38380;
XX
DT 29-AUG-2003 (revised)
DT 15-AUG-2002 (first entry)
XX
DE Chimeric sequence 6A8 from CMV promoters of human AD169/Towne strains.
XX
KW Immunomodulator; cytostatic; antibacterial; immunogenic; vaccination;
KW gene therapy; autoimmune disorder; tumour; chimeric; human; CMV promoter;
KW ds.
XX
OS Homo sapiens.
OS Chimeric.
XX
PN WO200200897-A2.
XX
PD 03-JAN-2002.
XX
PF 21-JUN-2001; 2001WO-US020123.
XX
PR 23-JUN-2000; 2000US-0213829P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Punnonen J, Wright A, Semyonov A;
XX
DR WPI; 2002-188381/24.
XX
PT New isolated or recombinant promoter/enhancers, useful in producing a
PT prophylactic or therapeutic effect in humans, especially useful in gene
PT therapy for treating or preventing infectious diseases, autoimmune
PT disorders or tumors.
XX
PS Claim 1; Fig 8; 110pp; English.
XX
CC The invention relates to isolated or recombinant nucleic acids, which
CC comprise any of 18 sequences fully defined in the specification. The
CC nucleic acids are designated 10B2, 11E2, 12C9, 12E1, 12H9, 3C9, 4B5, 6A8,

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 09:23:32 ; Search time 9389.39 Seconds
(without alignments)
10697.432 Million cell updates/sec

Title: US-09-886-942-8
Perfect score: 1767
Sequence: 1 atatgaggctatatcgccga.....tttctgcagtcaccgtcctt 1767

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	5	1741.4	98.6	229483	13	AC146851	AC146851 Human Her
c	6	1741.4	98.6	231236	13	AY315197	AY315197 Human her
	7	1728.6	97.8	1767	6	AX402393	AX402393 Sequence
	8	1728.6	97.8	1767	6	AX402403	AX402403 Sequence
	9	1727	97.7	1767	6	AX402404	AX402404 Sequence
	10	1725.4	97.6	1767	6	AX402402	AX402402 Sequence
	11	1720.6	97.4	1767	6	AX402406	AX402406 Sequence
	12	1714.2	97.0	1765	6	AX402401	AX402401 Sequence
	13	1704.6	96.5	229209	13	AC146907	AC146907 Human Her
c	14	1699.8	96.2	25556	13	AY446871	AY446871 Human her
	15	1699.8	96.2	226889	13	AC146905	AC146905 Human Her
	16	1698.8	96.1	1766	6	AX402394	AX402394 Sequence
c	17	1695.2	95.9	2129	6	A01324	A01324 Human cytom
	18	1695.2	95.9	2133	6	A01323	A01323 Human cytom
	19	1695.2	95.9	11795	6	AX027785	AX027785 Sequence
	20	1695.2	95.9	13254	6	AR038307	AR038307 Sequence
c	21	1695.2	95.9	13254	6	AR038321	AR038321 Sequence
	22	1695.2	95.9	13254	6	I58596	I58596 Sequence 15
c	23	1695.2	95.9	13254	6	I58610	I58610 Sequence 17
c	24	1695.2	95.9	229354	6	AR474465	AR474465 Sequence
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	32	1681.6	95.2	1767	6	AX402407	AX402407 Sequence
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c	35	1672.6	94.7	24589	13	AY446870	AY446870 Human her
c	36	1671.2	94.6	234881	13	AC146906	AC146906 Human Her
	37	1669.8	94.5	1757	6	AX402405	AX402405 Sequence
c	38	1666.2	94.3	25591	13	AY446865	AY446865 Human her
	39	1665	94.2	1757	6	AX402399	AX402399 Sequence
c	40	1665	94.2	25616	13	AY446864	AY446864 Human her
	41	1662.2	94.1	1758	6	AX402390	AX402390 Sequence
c	42	1638.4	92.7	235645	13	AY446894	AY446894 Human her
c	43	1636	92.6	25770	13	AY446868	AY446868 Human her
c	44	1625	92.0	25489	13	AY446867	AY446867 Human her
	45	1625	92.0	229700	13	AC146904	AC146904 Human Her

ALIGNMENTS

RESULT 1
AX402396
LOCUS AX402396 1767 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 8 from Patent WO0200897.
ACCESSION AX402396
VERSION AX402396.1 GI:21387431
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Punnonen,J., Wright,A. and Semyonov,A.
TITLE Novel chimeric promoters
JOURNAL Patent: WO 0200897-A 8 03-JAN-2002;
Maxygen, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1767
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
ORIGIN

Query Match 100.0%; Score 1767; DB 6; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ATCTATACATTGAATCAATATTGGCAATTAGCCATATTATTCATTGGTTATATAGCATAA 120
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Qy        121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCCGTATCATAATATGTACATTTAT 180
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Db        121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCCGTATCATAATATGTACATTTAT 180

Qy        181 ATTGGCCCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 15:25:23 ; Search time 429.506 Seconds
(without alignments)
3447.855 Million cell updates/sec

Title: US-09-886-942-8
Perfect score: 1767
Sequence: 1 atatgaggctatatcgccga.....tttctgcagtcaccgtcctt 1767

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6068529 seqs, 419036697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1695.2	95.9	8251	7	US-10-521-768-2	Sequence 2, Appli
2	1695.2	95.9	13535	7	US-10-521-768-4	Sequence 4, Appli
3	1603.6	90.8	7003	8	US-11-038-933-1	Sequence 1, Appli
4	1603.6	90.8	7073	8	US-11-038-933-2	Sequence 2, Appli
5	1603.6	90.8	7272	8	US-11-038-933-4	Sequence 4, Appli
6	1603.6	90.8	7285	8	US-11-038-933-3	Sequence 3, Appli
7	1585.8	89.7	5302	7	US-10-401-386B-81	Sequence 81, Appl
8	1579	89.4	5089	8	US-11-179-798-2	Sequence 2, Appli
9	1579	89.4	5089	8	US-11-179-798-5	Sequence 5, Appli
10	1579	89.4	5488	8	US-11-179-798-3	Sequence 3, Appli
11	1579	89.4	5488	8	US-11-179-798-6	Sequence 6, Appli
12	1579	89.4	5500	8	US-11-179-798-1	Sequence 1, Appli
13	1579	89.4	5500	8	US-11-179-798-4	Sequence 4, Appli
14	1576.4	89.2	10369	7	US-10-521-768-3	Sequence 3, Appli
15	1574.4	89.1	3547	8	US-11-115-425-100	Sequence 100, App
16	1572.8	89.0	4432	8	US-11-115-425-12	Sequence 12, Appl
17	1572.8	89.0	4864	8	US-11-115-425-14	Sequence 14, Appl
18	1572.4	89.0	2196	8	US-11-115-425-13	Sequence 13, Appl
19	1565.2	88.6	6245	7	US-10-401-386B-61	Sequence 61, Appl
20	1521.8	86.1	12745	6	US-10-978-927-8	Sequence 8, Appli
21	1368.6	77.5	1848	6	US-10-978-927-32	Sequence 32, Appl
22	810.2	45.9	5041	8	US-11-193-750-6	Sequence 6, Appli
23	810.2	45.9	5043	8	US-11-193-750-5	Sequence 5, Appli
24	810.2	45.9	5101	8	US-11-193-750-4	Sequence 4, Appli
25	810.2	45.9	5924	8	US-11-193-750-3	Sequence 3, Appli
26	810.2	45.9	5982	8	US-11-193-750-2	Sequence 2, Appli
27	810.2	45.9	6233	8	US-11-193-750-10	Sequence 10, Appl
28	810.2	45.9	17402	8	US-11-193-750-8	Sequence 8, Appli
29	810.2	45.9	18116	8	US-11-193-750-7	Sequence 7, Appli
30	751.2	42.5	6741	6	US-10-813-646-21	Sequence 21, Appl
31	749.4	42.4	4775	7	US-10-401-386B-62	Sequence 62, Appl
32	748.8	42.4	3913	7	US-10-981-267-27	Sequence 27, Appl
33	748.2	42.3	5391	6	US-10-981-356A-44	Sequence 44, Appl
34	748.2	42.3	5391	8	US-11-096-046-44	Sequence 44, Appl
35	748.2	42.3	5391	8	US-11-106-820-21	Sequence 21, Appl
36	748.2	42.3	5988	8	US-11-159-919-17	Sequence 17, Appl
37	748.2	42.3	6135	6	US-10-981-356A-45	Sequence 45, Appl
38	748.2	42.3	6135	8	US-11-096-046-45	Sequence 45, Appl
39	748.2	42.3	6135	8	US-11-106-820-22	Sequence 22, Appl
40	748.2	42.3	7127	8	US-11-192-219-46	Sequence 46, Appl
41	748.2	42.3	7201	8	US-11-159-919-16	Sequence 16, Appl
42	748.2	42.3	7496	8	US-11-159-919-15	Sequence 15, Appl
c 43	736.4	41.7	33014	8	US-11-077-716-1	Sequence 1, Appli
44	734.8	41.6	9117	8	US-11-003-967-26	Sequence 26, Appl
45	734	41.5	6630	8	US-11-065-716-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-10-521-768-2
; Sequence 2, Application US/10521768
; Publication No. US20060003405A1
; GENERAL INFORMATION:
; APPLICANT: Lonza Biologics plc.
; TITLE OF INVENTION: Method of expressing recombinant protein in CHO cells
; FILE REFERENCE: 4145-22
; CURRENT APPLICATION NUMBER: US/10/521,768
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: PCT/EP2003/007946
; PRIOR FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: GB 0216648.6
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 8251
; TYPE: DNA
; ORGANISM: Hamster sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Seq. ID. No. 3: circular plasmid GS vector p12.4 hCMVp-GFP /clon
; OTHER INFORMATION: 13
US-10-521-768-2

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Matches 1729; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 10:33:48 ; Search time 343.801 Seconds
(without alignments)
9135.958 Million cell updates/sec

Title: US-09-886-942-8
Perfect score: 1767
Sequence: 1 atatgaggctatatcgccga.....tttctgcagtcaccgtccttt 1767

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1695.2	95.9	13254	6	PCT-US95-08743-156	Sequence 156, App
c 8	1695.2	95.9	13254	6	PCT-US95-08743-170	Sequence 170, App
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10	1692.8	95.8	2170	3	US-09-977-066A-4	Sequence 4, Appli
11	1620.6	91.7	4326	3	US-08-760-615-7	Sequence 7, Appli
12	1603.6	90.8	5108	3	US-09-628-730-51	Sequence 51, Appl
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14	1603.6	90.8	5111	3	US-09-628-730-55	Sequence 55, Appl
15	1603.6	90.8	5185	3	US-09-628-730-47	Sequence 47, Appl
16	1603.6	90.8	5188	3	US-09-628-730-59	Sequence 59, Appl
17	1603.6	90.8	5254	3	US-09-628-730-60	Sequence 60, Appl
18	1603.6	90.8	7003	3	US-09-913-909-1	Sequence 1, Appli
19	1603.6	90.8	7073	3	US-09-913-909-2	Sequence 2, Appli
20	1603.6	90.8	7272	3	US-09-913-909-4	Sequence 4, Appli
21	1603.6	90.8	7285	3	US-09-913-909-3	Sequence 3, Appli
22	1590.6	90.0	15538	3	US-09-554-337-1	Sequence 1, Appli
23	1581	89.5	4928	2	US-08-345-913-1	Sequence 1, Appli
24	1581	89.5	4928	3	US-08-818-562-1	Sequence 1, Appli
25	1581	89.5	4928	3	US-09-628-445-1	Sequence 1, Appli
26	1574.4	89.1	3547	3	US-09-340-798A-43	Sequence 43, Appl
27	1574.4	89.1	3610	3	US-09-194-949A-1	Sequence 1, Appli
28	1574.4	89.1	4261	3	US-09-194-949A-25	Sequence 25, Appl
29	1572.8	89.0	4864	3	US-09-340-798A-1	Sequence 1, Appli
30	1570.2	88.9	5899	3	US-09-173-053-2	Sequence 2, Appli
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33	1560.8	88.3	5845	3	US-09-173-053-1	Sequence 1, Appli
34	1560.8	88.3	5900	2	US-08-663-998-1	Sequence 1, Appli
35	1560.8	88.3	5952	2	US-08-663-998-2	Sequence 2, Appli
36	1556.2	88.1	4915	3	US-09-173-053-7	Sequence 7, Appli
37	1554.2	88.0	4276	3	US-09-721-480-1	Sequence 1, Appli
38	1554.2	88.0	5128	3	US-09-721-480-2	Sequence 2, Appli
39	1554.2	88.0	5459	3	US-09-721-480-4	Sequence 4, Appli
40	1554.2	88.0	5882	3	US-09-721-480-6	Sequence 6, Appli
41	1553	87.9	5215	3	US-09-173-053-8	Sequence 8, Appli
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44	1547.8	87.6	4328	3	US-09-132-808-1	Sequence 1, Appli
45	1547.8	87.6	4328	3	US-08-910-647-2	Sequence 2, Appli

ALIGNMENTS

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US-08-276-852-156
; Sequence 156, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 09:23:32 ; Search time 4830.2 Seconds
(without alignments)
10697.432 Million cell updates/sec

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Perfect score: 909
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 11766282

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	6	899.4	98.9	231236	13	AY315197	AY315197 Human her
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	12	891.4	98.1	2133	6	A01323	A01323 Human cytom
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	14	891.4	98.1	11795	6	AX027785	AX027785 Sequence
	15	891.4	98.1	13254	6	AR038307	AR038307 Sequence
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	17	891.4	98.1	13254	6	I58596	I58596 Sequence 15
c	18	891.4	98.1	13254	6	I58610	I58610 Sequence 17
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	31	880.2	96.8	229209	13	AC146907	AC146907 Human Her
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ALIGNMENTS

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LOCUS AX402396 1767 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 8 from Patent WO0200897.
ACCESSION AX402396
VERSION AX402396.1 GI:21387431
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Punnonen,J., Wright,A. and Semyonov,A.
TITLE Novel chimeric promoters
JOURNAL Patent: WO 0200897-A 8 03-JAN-2002;
Maxygen, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1767
/organism="synthetic construct"
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/note="Synthetic oligonucleotide"
ORIGIN

Query Match 100.0%; Score 909; DB 6; Length 1767;
Best Local Similarity 100.0%; Pred. No. 1e-261;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ATCTATACATTGAATCAATATTGGCAATTAGCCATATTATTCATTGGTTATATAGCATAA 120
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Db         61 ATCTATACATTGAATCAATATTGGCAATTAGCCATATTATTCATTGGTTATATAGCATAA 120

Qy        121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCCGTATCATAATATGTACATTTAT 180
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Qy        181 ATTGGCCCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 09:16:57 ; Search time 601.381 Seconds
(without alignments)
10073.821 Million cell updates/sec

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Perfect score: 909
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	909	100.0	4790	13	ADS20070	Ads20070 pMV10.1-C
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	6	897.8	98.8	6408	8	ABX10643	Abx10643 Vector, h
	7	897.8	98.8	6485	8	ABX10644	Abx10644 Vector, h
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	9	893	98.2	1767	6	AAL38377	Aal38377 Chimeric
	10	893	98.2	1767	6	AAL38387	Aal38387 Chimeric
	11	891.4	98.1	1848	8	ADA50596	Ada50596 HCMV imme
	12	891.4	98.1	1848	12	ADF53547	Adf53547 Human CMV
	13	891.4	98.1	2133	1	AAN91042	Aan91042 Promoter-
	14	891.4	98.1	6845	6	ABK37491	Abk37491 Vesicular
	15	891.4	98.1	7073	2	AAT50962	Aat50962 TF8-5G9 C
	16	891.4	98.1	7864	2	AAT50963	Aat50963 TF8-5G9 C
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	18	891.4	98.1	9831	14	AEB86488	Aeb86488 LAP vecto
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	21	891.4	98.1	13254	3	AAA32151	Aaa32151 pEe12 Com
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c	23	891.4	98.1	13254	3	AAA31039	Aaa31039 Complete
	24	891.4	98.1	13535	12	ADJ57067	Adj57067 Vector pl
c	25	891.4	98.1	229354	6	ABQ74179	Abq74179 Human cyt
	26	889.8	97.9	1767	6	AAL38386	Aal38386 Chimeric
	27	888.2	97.7	1767	6	AAL38373	Aal38373 Chimeric
	28	888.2	97.7	13254	3	AAA31025	Aaa31025 pEe12 Com
	29	885.8	97.4	1765	6	AAL38385	Aal38385 Chimeric
	30	885	97.4	1767	6	AAL38390	Aal38390 Chimeric
	31	883.6	97.2	1766	6	AAL38378	Aal38378 Chimeric
	32	879.4	96.7	1767	6	AAL38391	Aal38391 Wild-type
	33	874.8	96.2	912	2	AAZ09519	Aaz09519 Human CMV
	34	874.8	96.2	1765	6	AAL38392	Aal38392 Wild-type
	35	874.8	96.2	2170	6	AAD38152	Aad38152 Human cyt
	36	874.8	96.2	2361	8	ADA50595	Ada50595 HCMV imme
	37	874.8	96.2	2361	14	ADW07232	Adw07232 DNA seque
	38	867.4	95.4	8083	2	AAQ90132	Aaq90132 Plasmid p
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	40	867.4	95.4	8135	2	AAQ90136	Aaq90136 Plasmid p
c	41	867.4	95.4	8149	2	AAQ90133	Aaq90133 Plasmid p
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ALIGNMENTS

RESULT 1
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ID AAL38380 standard; DNA; 1767 BP.
XX
AC AAL38380;
XX
DT 29-AUG-2003 (revised)
DT 15-AUG-2002 (first entry)
XX
DE Chimeric sequence 6A8 from CMV promoters of human AD169/Towne strains.
XX
KW Immunomodulator; cytostatic; antibacterial; immunogenic; vaccination;
KW gene therapy; autoimmune disorder; tumour; chimeric; human; CMV promoter;
KW ds.
XX
OS Homo sapiens.
OS Chimeric.
XX
PN WO200200897-A2.
XX
PD 03-JAN-2002.
XX
PF 21-JUN-2001; 2001WO-US020123.
XX
PR 23-JUN-2000; 2000US-0213829P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Punnonen J, Wright A, Semyonov A;
XX
DR WPI; 2002-188381/24.
XX
PT New isolated or recombinant promoter/enhancers, useful in producing a
PT prophylactic or therapeutic effect in humans, especially useful in gene
PT therapy for treating or preventing infectious diseases, autoimmune
PT disorders or tumors.
XX
PS Claim 1; Fig 8; 110pp; English.
XX
CC The invention relates to isolated or recombinant nucleic acids, which
CC comprise any of 18 sequences fully defined in the specification. The
CC nucleic acids are designated 10B2, 11E2, 12C9, 12E1, 12H9, 3C9, 4B5, 6A8,

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 15:25:23 ; Search time 220.951 Seconds
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3447.855 Million cell updates/sec

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	810.2	89.1	5043	8	US-11-193-750-5	Sequence 5, Appli
6	810.2	89.1	5101	8	US-11-193-750-4	Sequence 4, Appli
7	810.2	89.1	5924	8	US-11-193-750-3	Sequence 3, Appli
8	810.2	89.1	5982	8	US-11-193-750-2	Sequence 2, Appli
9	810.2	89.1	6233	8	US-11-193-750-10	Sequence 10, Appl
10	810.2	89.1	17402	8	US-11-193-750-8	Sequence 8, Appli
11	810.2	89.1	18116	8	US-11-193-750-7	Sequence 7, Appli
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13	770.6	84.8	3547	8	US-11-115-425-100	Sequence 100, App
14	769	84.6	4432	8	US-11-115-425-12	Sequence 12, Appl
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24	763	83.9	5488	8	US-11-179-798-3	Sequence 3, Appli
25	763	83.9	5488	8	US-11-179-798-6	Sequence 6, Appli
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33	714.4	78.6	4800	7	US-10-855-490C-49	Sequence 49, Appl
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36	690	75.9	5391	8	US-11-096-046-44	Sequence 44, Appl
37	690	75.9	5391	8	US-11-106-820-21	Sequence 21, Appl
38	690	75.9	5988	8	US-11-159-919-17	Sequence 17, Appl
39	690	75.9	6135	6	US-10-981-356A-45	Sequence 45, Appl
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42	690	75.9	6741	6	US-10-813-646-21	Sequence 21, Appl
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ALIGNMENTS

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; Publication No. US20060009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; TITLE OF INVENTION: BETA-HEXOSAMINIDASE
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-32

Query Match 98.1%; Score 891.4; DB 6; Length 1848;
Best Local Similarity 98.8%; Pred. No. 1.7e-265;
Matches 898; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	909	100.0	1767	3	US-09-886-942-8	Sequence 8, Appli
2	909	100.0	3879	7	US-10-446-629-2	Sequence 2, Appli
3	909	100.0	4790	7	US-10-446-629-3	Sequence 3, Appli
4	899.4	98.9	1767	3	US-09-886-942-21	Sequence 21, Appl
c 5	899.4	98.9	218802	9	US-10-897-508-1	Sequence 1, Appli
6	897.8	98.8	6408	3	US-09-996-128A-1	Sequence 1, Appli
7	897.8	98.8	6485	3	US-09-996-128A-2	Sequence 2, Appli
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9	893	98.2	1767	3	US-09-886-942-15	Sequence 15, Appl
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13	891.4	98.1	6845	8	US-10-838-906-26	Sequence 26, Appl
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17	885.8	97.4	1765	3	US-09-886-942-13	Sequence 13, Appl
18	885	97.4	1767	3	US-09-886-942-18	Sequence 18, Appl
19	883.6	97.2	1766	3	US-09-886-942-6	Sequence 6, Appli
20	879.4	96.7	1767	3	US-09-886-942-19	Sequence 19, Appl
21	874.8	96.2	912	6	US-10-223-507-52	Sequence 52, Appl
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34	858.4	94.4	3570	10	US-11-126-465-1	Sequence 1, Appli
35	839	92.3	1757	3	US-09-886-942-17	Sequence 17, Appl
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37	831	91.4	1757	3	US-09-886-942-11	Sequence 11, Appl
38	827.4	91.0	897	3	US-09-886-942-3	Sequence 3, Appli
39	821	90.3	930	5	US-10-206-747-2	Sequence 2, Appli
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ALIGNMENTS

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; Sequence 8, Application US/09886942
; Patent No. US20020081708A1
; GENERAL INFORMATION:
;    APPLICANT:  PUNNONEN, JUHA
;    WRIGHT, ANNE
;    SEMYONOV, ANDREY
;  APPLICANT:
;  TITLE OF INVENTION: NOVEL CHIMERIC PROMOTERS
;  FILE REFERENCE: 02-031910US
;  CURRENT APPLICATION NUMBER: US/09/886,942
;  CURRENT FILING DATE:  2001-06-21
;  PRIOR APPLICATION NUMBER: 60/213,829
;  PRIOR FILING DATE: 2000-06-23
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 1767
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-886-942-8

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  Best Local Similarity  100.0%;  Pred. No. 1.2e-249;
  Matches  909;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 ATTGGCCCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

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9135.958 Million cell updates/sec

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Scoring table: IDENTITY_NUC
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Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	891.4	98.1	13254	2	US-08-899-575-156	Sequence 156, App
c 4	891.4	98.1	13254	2	US-08-899-575-170	Sequence 170, App
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7	891.4	98.1	13254	6	PCT-US95-08743-156	Sequence 156, App
c 8	891.4	98.1	13254	6	PCT-US95-08743-170	Sequence 170, App
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10	874.8	96.2	912	3	US-09-495-052-52	Sequence 52, Appl
11	874.8	96.2	2170	3	US-09-977-066A-4	Sequence 4, Appli
12	858.4	94.4	3570	3	US-09-881-457A-1	Sequence 1, Appli
13	845.4	93.0	874	3	US-09-051-696-4	Sequence 4, Appli
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18	821	90.3	930	2	US-07-972-135-2	Sequence 2, Appli
19	821	90.3	930	2	US-07-972-135-4	Sequence 4, Appli
20	821	90.3	930	3	US-08-256-004-2	Sequence 2, Appli
21	821	90.3	930	3	US-09-006-841-2	Sequence 2, Appli
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25	821	90.3	930	3	US-09-132-391-4	Sequence 4, Appli
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30	787	86.6	4207	3	US-09-897-511A-4	Sequence 4, Appli
31	787	86.6	4210	3	US-09-897-511A-5	Sequence 5, Appli
32	787	86.6	6255	3	US-09-897-511A-13	Sequence 13, Appl
33	786.4	86.5	7352	3	US-08-786-531B-4	Sequence 4, Appli
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35	786.4	86.5	8560	3	US-09-936-572-11	Sequence 11, Appl
36	786.4	86.5	9511	3	US-09-897-511A-34	Sequence 34, Appl
37	786.4	86.5	11299	3	US-09-238-356-14	Sequence 14, Appl
38	780.6	85.9	4326	3	US-08-760-615-7	Sequence 7, Appli
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ALIGNMENTS

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; Sequence 156, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 156:
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; LENGTH: 13254 base pairs
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; STRANDEDNESS: double

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 09:23:32 ; Search time 4952.41 Seconds
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Post-processing: Minimum Match 0%
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14: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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VERSION AX402409.1 GI:21387444
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
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AUTHORS Punnonen,J., Wright,A. and Semyonov,A.
TITLE Novel chimeric promoters
JOURNAL Patent: WO 0200897-A 21 03-JAN-2002;
Maxygen, Inc. (US)
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Qy         61 ATCTATACATTGAATCAATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATAA 120
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Qy        121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTAT 180
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Db        121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTAT 180

Qy        181 ATTGGCTCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 09:16:57 ; Search time 616.598 Seconds
(without alignments)
10073.821 Million cell updates/sec

Title: US-09-886-942-21_COPY_1_932
Perfect score: 932
Sequence: 1 atatgaggctatatcgccga.....ccccgtgccaagagtgacgt 932

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	932	100.0	1767	6	AAL38393	Aal38393 Consensus
c	2	932	100.0	218802	14	ADW98820	Adw98820 Human her
	3	930.4	99.8	6408	8	ABX10643	Abx10643 Vector, h
	4	930.4	99.8	6485	8	ABX10644	Abx10644 Vector, h
	5	925.6	99.3	1767	6	AAL38387	Aal38387 Chimeric
	6	922.4	99.0	1767	6	AAL38377	Aal38377 Chimeric
	7	922.4	99.0	1767	6	AAL38386	Aal38386 Chimeric
	8	922.4	99.0	1767	6	AAL38380	Aal38380 Chimeric
	9	922.4	99.0	3879	13	ADS20069	Ads20069 pMV10.1-s
	10	922.4	99.0	4790	13	ADS20070	Ads20070 pMV10.1-C
	11	920.8	98.8	1767	6	AAL38388	Aal38388 Chimeric
	12	920.8	98.8	1767	6	AAL38373	Aal38373 Chimeric
	13	916	98.3	1767	6	AAL38390	Aal38390 Chimeric
	14	914.4	98.1	1848	8	ADA50596	Ada50596 HCMV imme
	15	914.4	98.1	1848	12	ADF53547	Adf53547 Human CMV
	16	914.4	98.1	2133	1	AAN91042	Aan91042 Promoter-
	17	914.4	98.1	6845	6	ABK37491	Abk37491 Vesicular
	18	914.4	98.1	7073	2	AAT50962	Aat50962 TF8-5G9 C
	19	914.4	98.1	7864	2	AAT50963	Aat50963 TF8-5G9 C
	20	914.4	98.1	8251	12	ADJ57065	Adj57065 Vector pl
	21	914.4	98.1	9831	14	AEB86488	Aeb86488 LAP vecto
	22	914.4	98.1	11795	3	AAA59345	Aaa59345 Nucleotid
	23	914.4	98.1	13254	2	AAT40915	Aat40915 Nucleotid
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	27	914.4	98.1	13535	12	ADJ57067	Adj57067 Vector pl
c	28	914.4	98.1	229354	6	ABQ74179	Abq74179 Human cyt
	29	913	98.0	1766	6	AAL38378	Aal38378 Chimeric
	30	911.2	97.8	13254	3	AAA31025	Aaa31025 pEe12 Com
	31	907.4	97.4	1765	6	AAL38392	Aal38392 Wild-type
	32	907.4	97.4	2170	6	AAD38152	Aad38152 Human cyt
	33	907.4	97.4	2361	8	ADA50595	Ada50595 HCMV imme
	34	907.4	97.4	2361	14	ADW07232	Adw07232 DNA seque
	35	902.4	96.8	1767	6	AAL38391	Aal38391 Wild-type
	36	896.6	96.2	1765	6	AAL38385	Aal38385 Chimeric
	37	887.4	95.2	912	2	AAZ09519	Aaz09519 Human CMV
	38	868.4	93.2	1757	6	AAL38389	Aal38389 Chimeric
	39	868	93.1	3570	6	ABK90556	Abk90556 Newcastle
	40	867.4	93.1	8083	2	AAQ90132	Aaq90132 Plasmid p
c	41	867.4	93.1	8135	2	AAQ90134	Aaq90134 Plasmid p
	42	867.4	93.1	8135	2	AAQ90136	Aaq90136 Plasmid p
c	43	867.4	93.1	8149	2	AAQ90133	Aaq90133 Plasmid p
	44	867.4	93.1	8149	2	AAQ90135	Aaq90135 Plasmid p
	45	864.4	92.7	8687	6	ABV72727	Abv72727 Expressio

ALIGNMENTS

RESULT 1
AAL38393
ID AAL38393 standard; DNA; 1767 BP.
XX
AC AAL38393;
XX
DT 15-AUG-2002 (first entry)
XX
DE Consensus sequence of AD169 and Towne CMV promoters.
XX
KW Immunomodulator; cytostatic; antibacterial; immunogenic; vaccination;
KW gene therapy; autoimmune disorder; tumour; CMV promoter; human;
KW wild-type; ds.
XX
OS Unidentified.
XX
PN WO200200897-A2.
XX
PD 03-JAN-2002.
XX
PF 21-JUN-2001; 2001WO-US020123.
XX
PR 23-JUN-2000; 2000US-0213829P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Punnonen J, Wright A, Semyonov A;
XX
DR WPI; 2002-188381/24.
XX
PT New isolated or recombinant promoter/enhancers, useful in producing a
PT prophylactic or therapeutic effect in humans, especially useful in gene
PT therapy for treating or preventing infectious diseases, autoimmune
PT disorders or tumors.
XX
PS Disclosure; Fig 8; 110pp; English.
XX
CC The invention relates to isolated or recombinant nucleic acids, which
CC comprise any of 18 sequences fully defined in the specification. The
CC nucleic acids are designated 10B2, 11E2, 12C9, 12E1, 12H9, 3C9, 4B5, 6A8,
CC 6B2, 6D4, 6F6, 9E1, 9F11, 9G11, 9G12, 9G4, 9G7 and 9G8, and comprise 898-
CC 1768 base pair sequences. The nucleic acids are useful in producing an

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 13:11:03 ; Search time 1096.8 Seconds
(without alignments)
7026.829 Million cell updates/sec

Title: US-09-886-942-21_COPY_1_932
Perfect score: 932
Sequence: 1 atatgaggctatatcgccga.....ccccgtgccaagagtgacgt 932

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	932	100.0	1767	3	US-09-886-942-21	Sequence 21, Appl
c 2	932	100.0	218802	9	US-10-897-508-1	Sequence 1, Appli
3	930.4	99.8	6408	3	US-09-996-128A-1	Sequence 1, Appli
4	930.4	99.8	6485	3	US-09-996-128A-2	Sequence 2, Appli
5	925.6	99.3	1767	3	US-09-886-942-15	Sequence 15, Appl
6	922.4	99.0	1767	3	US-09-886-942-5	Sequence 5, Appli
7	922.4	99.0	1767	3	US-09-886-942-8	Sequence 8, Appli
8	922.4	99.0	1767	3	US-09-886-942-14	Sequence 14, Appl
9	922.4	99.0	3879	7	US-10-446-629-2	Sequence 2, Appli
10	922.4	99.0	4790	7	US-10-446-629-3	Sequence 3, Appli
11	920.8	98.8	1767	3	US-09-886-942-16	Sequence 16, Appl
12	916	98.3	1767	3	US-09-886-942-18	Sequence 18, Appl
13	914.4	98.1	1848	8	US-10-781-142-32	Sequence 32, Appl
14	914.4	98.1	6845	5	US-10-239-804-6	Sequence 6, Appli
15	914.4	98.1	6845	8	US-10-838-906-26	Sequence 26, Appl
16	914.4	98.1	13254	6	US-10-016-986-156	Sequence 156, App
c 17	914.4	98.1	13254	6	US-10-016-986-170	Sequence 170, App
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19	907.4	97.4	1665	3	US-09-886-942-20	Sequence 20, Appl
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21	907.4	97.4	2170	10	US-11-103-805-4	Sequence 4, Appli
22	902.4	96.8	1767	3	US-09-886-942-19	Sequence 19, Appl
23	896.6	96.2	1765	3	US-09-886-942-13	Sequence 13, Appl
24	887.4	95.2	912	6	US-10-223-507-52	Sequence 52, Appl
25	868.4	93.2	1757	3	US-09-886-942-17	Sequence 17, Appl
26	868	93.1	3570	3	US-09-881-457A-1	Sequence 1, Appli
27	868	93.1	3570	10	US-11-126-465-1	Sequence 1, Appli
28	864.4	92.7	8687	7	US-10-467-546-15	Sequence 15, Appl
29	864.4	92.7	8687	7	US-10-467-546-16	Sequence 16, Appl
30	864.4	92.7	8687	9	US-10-666-332-15	Sequence 15, Appl
31	864.4	92.7	8687	9	US-10-666-332-16	Sequence 16, Appl
32	864.4	92.7	9362	7	US-10-467-546-18	Sequence 18, Appl
33	864.4	92.7	9362	9	US-10-666-332-18	Sequence 18, Appl
34	864.4	92.7	9400	7	US-10-467-546-17	Sequence 17, Appl
35	864.4	92.7	9400	9	US-10-666-332-17	Sequence 17, Appl
36	859.2	92.2	1758	3	US-09-886-942-2	Sequence 2, Appli
37	857.2	92.0	1757	3	US-09-886-942-11	Sequence 11, Appl
38	842.4	90.4	930	5	US-10-206-747-2	Sequence 2, Appli
39	842.4	90.4	930	5	US-10-206-747-4	Sequence 4, Appli
40	830.6	89.1	897	3	US-09-886-942-3	Sequence 3, Appli
41	815	87.4	5041	8	US-10-790-455-6	Sequence 6, Appli
42	815	87.4	5041	8	US-10-811-136B-6	Sequence 6, Appli
43	815	87.4	5041	8	US-10-940-315-6	Sequence 6, Appli
44	815	87.4	5041	9	US-10-950-050-6	Sequence 6, Appli
45	815	87.4	5041	10	US-11-068-155-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
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; Sequence 21, Application US/09886942
; Patent No. US20020081708A1
; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA
; WRIGHT, ANNE
; SEMYONOV, ANDREY
; APPLICANT:
; TITLE OF INVENTION: NOVEL CHIMERIC PROMOTERS
; FILE REFERENCE: 02-031910US
; CURRENT APPLICATION NUMBER: US/09/886,942
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/213,829
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: sequence
US-09-886-942-21

Query Match 100.0%; Score 932; DB 3; Length 1767;
Best Local Similarity 100.0%; Pred. No. 4.9e-253;
Matches 932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        181 ATTGGCTCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 15:25:23 ; Search time 226.542 Seconds
(without alignments)
3447.855 Million cell updates/sec

Title: US-09-886-942-21_COPY_1_932
Perfect score: 932
Sequence: 1 atatgaggctatatcgccga.....ccccgtgccaagagtgacgt 932

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6068529 seqs, 419036697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	914.4	98.1	13535	7	US-10-521-768-4	Sequence 4, Appli
4	815	87.4	5041	8	US-11-193-750-6	Sequence 6, Appli
5	815	87.4	5043	8	US-11-193-750-5	Sequence 5, Appli
6	815	87.4	5101	8	US-11-193-750-4	Sequence 4, Appli
7	815	87.4	5924	8	US-11-193-750-3	Sequence 3, Appli
8	815	87.4	5982	8	US-11-193-750-2	Sequence 2, Appli
9	815	87.4	6233	8	US-11-193-750-10	Sequence 10, Appl
10	815	87.4	17402	8	US-11-193-750-8	Sequence 8, Appli
11	815	87.4	18116	8	US-11-193-750-7	Sequence 7, Appli
12	795.6	85.4	10369	7	US-10-521-768-3	Sequence 3, Appli
13	794	85.2	6245	7	US-10-401-386B-61	Sequence 61, Appl
14	793.6	85.2	3547	8	US-11-115-425-100	Sequence 100, App
15	792.4	85.0	5089	8	US-11-179-798-2	Sequence 2, Appli
16	792.4	85.0	5089	8	US-11-179-798-5	Sequence 5, Appli
17	792.4	85.0	5488	8	US-11-179-798-3	Sequence 3, Appli
18	792.4	85.0	5488	8	US-11-179-798-6	Sequence 6, Appli
19	792.4	85.0	5500	8	US-11-179-798-1	Sequence 1, Appli
20	792.4	85.0	5500	8	US-11-179-798-4	Sequence 4, Appli
21	792	85.0	4432	8	US-11-115-425-12	Sequence 12, Appl
22	792	85.0	4864	8	US-11-115-425-14	Sequence 14, Appl
23	792	85.0	7003	8	US-11-038-933-1	Sequence 1, Appli
24	792	85.0	7073	8	US-11-038-933-2	Sequence 2, Appli
25	792	85.0	7272	8	US-11-038-933-4	Sequence 4, Appli
26	792	85.0	7285	8	US-11-038-933-3	Sequence 3, Appli
27	791.6	84.9	2196	8	US-11-115-425-13	Sequence 13, Appl
28	782.6	84.0	5302	7	US-10-401-386B-81	Sequence 81, Appl
29	757.4	81.3	4775	7	US-10-401-386B-62	Sequence 62, Appl
30	739.6	79.4	9117	8	US-11-003-967-26	Sequence 26, Appl
31	738.8	79.3	6630	8	US-11-065-716-51	Sequence 51, Appl
32	734.2	78.8	12745	6	US-10-978-927-8	Sequence 8, Appli
33	719.2	77.2	1022	8	US-11-118-855-2	Sequence 2, Appli
34	719.2	77.2	4800	7	US-10-855-490C-49	Sequence 49, Appl
35	711.4	76.3	5391	6	US-10-981-356A-44	Sequence 44, Appl
36	711.4	76.3	5391	8	US-11-096-046-44	Sequence 44, Appl
37	711.4	76.3	5391	8	US-11-106-820-21	Sequence 21, Appl
38	711.4	76.3	5988	8	US-11-159-919-17	Sequence 17, Appl
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42	711.4	76.3	6741	6	US-10-813-646-21	Sequence 21, Appl
43	711.4	76.3	7127	8	US-11-192-219-46	Sequence 46, Appl
44	711.4	76.3	7201	8	US-11-159-919-16	Sequence 16, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 32, Application US/10978927
; Publication No. US20060009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; TITLE OF INVENTION: BETA-HEXOSAMINIDASE
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-32

Query Match 98.1%; Score 914.4; DB 6; Length 1848;
Best Local Similarity 98.8%; Pred. No. 8.4e-268;
Matches 921; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy         61 ATCTATACATTGAATCAATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATAA 120
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Qy        121 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTAT 180
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Db        453 ATCAATATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTTAT 512

Qy        181 ATTGGCTCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 240
              |||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||
Db        513 ATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAG 572
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 10:33:48 ; Search time 181.337 Seconds
(without alignments)
9135.958 Million cell updates/sec

Title: US-09-886-942-21_COPY_1_932
Perfect score: 932
Sequence: 1 atatgaggctatatcgccga.....ccccgtgccaagagtgacgt 932

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	914.4	98.1	13254	2	US-08-276-852-156	Sequence 156, App
c 2	914.4	98.1	13254	2	US-08-276-852-170	Sequence 170, App
3	914.4	98.1	13254	2	US-08-899-575-156	Sequence 156, App
c 4	914.4	98.1	13254	2	US-08-899-575-170	Sequence 170, App
5	914.4	98.1	13254	2	US-08-899-575-156	Sequence 156, App
c 6	914.4	98.1	13254	2	US-08-899-575-170	Sequence 170, App
7	914.4	98.1	13254	6	PCT-US95-08743-156	Sequence 156, App
c 8	914.4	98.1	13254	6	PCT-US95-08743-170	Sequence 170, App
c 9	914.4	98.1	229354	3	US-09-705-400-64	Sequence 64, Appl
10	907.4	97.4	2170	3	US-09-977-066A-4	Sequence 4, Appli
11	887.4	95.2	912	3	US-09-495-052-52	Sequence 52, Appl
12	868	93.1	3570	3	US-09-881-457A-1	Sequence 1, Appli
13	850	91.2	874	3	US-09-051-696-4	Sequence 4, Appli
14	842.4	90.4	930	2	US-08-029-022-2	Sequence 2, Appli
15	842.4	90.4	930	2	US-08-029-022-4	Sequence 4, Appli
16	842.4	90.4	930	2	US-08-246-376-2	Sequence 2, Appli
17	842.4	90.4	930	2	US-08-246-376-4	Sequence 4, Appli
18	842.4	90.4	930	2	US-07-972-135-2	Sequence 2, Appli
19	842.4	90.4	930	2	US-07-972-135-4	Sequence 4, Appli
20	842.4	90.4	930	3	US-08-256-004-2	Sequence 2, Appli
21	842.4	90.4	930	3	US-09-006-841-2	Sequence 2, Appli
22	842.4	90.4	930	3	US-09-006-841-4	Sequence 4, Appli
23	842.4	90.4	930	3	US-09-461-686-2	Sequence 2, Appli
24	842.4	90.4	930	3	US-09-132-391-2	Sequence 2, Appli
25	842.4	90.4	930	3	US-09-132-391-4	Sequence 4, Appli
26	842.4	90.4	930	3	US-09-090-030-2	Sequence 2, Appli
27	842.4	90.4	930	3	US-09-090-030-4	Sequence 4, Appli
28	842.4	90.4	930	6	PCT-US93-05366-2	Sequence 2, Appli
29	842.4	90.4	930	6	PCT-US93-05366-4	Sequence 4, Appli
30	810	86.9	4326	3	US-08-760-615-7	Sequence 7, Appli
31	807.4	86.6	4276	3	US-09-721-480-1	Sequence 1, Appli
32	807.4	86.6	5128	3	US-09-721-480-2	Sequence 2, Appli
33	807.4	86.6	5459	3	US-09-721-480-4	Sequence 4, Appli
34	807.4	86.6	5882	3	US-09-721-480-6	Sequence 6, Appli
35	801.4	86.0	9600	3	US-08-910-647-1	Sequence 1, Appli
36	801.4	86.0	9600	3	US-09-620-925-1	Sequence 1, Appli
37	801	85.9	4328	3	US-09-132-808-1	Sequence 1, Appli
38	801	85.9	4328	3	US-08-910-647-2	Sequence 2, Appli
39	801	85.9	4328	3	US-09-620-925-2	Sequence 2, Appli
40	801	85.9	4328	3	US-09-620-260-1	Sequence 1, Appli
41	801	85.9	4328	3	US-09-620-259-1	Sequence 1, Appli
42	801	85.9	4818	3	US-08-910-647-4	Sequence 4, Appli
43	801	85.9	4818	3	US-09-620-925-4	Sequence 4, Appli
44	801	85.9	5107	3	US-08-910-647-3	Sequence 3, Appli
45	801	85.9	5107	3	US-09-620-925-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-276-852-156
; Sequence 156, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double